Search Strategy

FILE 'USPATFULL' ENTERED AT 12:03:51 ON 05 DEC 2002

		E	ALIZON MARC/IN
L1	43	S	E3
L2	43	S	L1 AND (ENV OR ENVELOPE)
L3	26	S	L2 AND (ENV/CLM OR ENVELOPE/CLM)
L4	13	S	L3 NOT (HIV-2)
L5	6473	S	(HIV-1 OR HUMAN IMMUNODEFICIENCY VIRUS TYPE 1)
L6	5626	S	L5 AND (ISOLATE? OR VARIANT? OR CLONE?)
L7	2520	S	L6 AND (NUCLEOTIDE SEQUENCE?)
L8	1345	S	L7 AND (ENV OR ENVELOPE OR GP120 OR GP160 OR GP41)
L9	140	S	L8 AND (COMPLETE NUCLEOTIDE SEQUENCE OR SEQUENCED (5W) ENTIRE
L10	40	S	L9 AND (ENV/CLM OR ENVELOPE/CLM)
L11	36	S	L10 NOT L1

FILE 'MEDLINE' ENTERED AT 12:18:28 ON 05 DEC 2002

		E	ALIZON MARC/AU
L12	67	S	E2-E3
L13	38798	S	(HIV-1 OR HUMAN IMMUNODEFICIENCY VIRUS TYPE 1)
L14	7604	S	L13 AND (ISOLATE? OR VARIANT? OR VARIATION OR QUASISPECIES OR
L15	2675	S	L14 AND (ENV OR ENVELOPE)
L16	760	S	L15 AND (NUCLEOTIDE SEQUENCE OR DIVERGENCE OR DIVERSITY OR VA
L17	611	S	L16 AND VARIATION
L18	57	S	L17 AND PY=1998
L19	192	S	L17 AND (SEQUENCE DIVERSITY OR SEQUENCE ANALYSIS OR GENETIC D
L20	12	S	L19 AND PY=1995
L21	15	S	L19 AND PY=1993
L22	9	S	L19 AND CLADE?
L23	1	S	L19 AND (MAL OR ELI)

L4 ANSWER 1 OF 13 USPATFULL
2002:314652 Variant of LAV viruses.
Alizon, Marc, Paris, FRANCE
Sonigo, Pierre, Paris, FRANCE
Wain-Hobson, Simon, Montigny Les Bretonneux, FRANCE
Montagnier, Luc, Le Plessis Robinson, FRANCE
Institut Pasteur (non-U.S. corporation)
US 2002177128 A1 20021128
APPLICATION: US 2002-76370 A1 20020219 (10)
PRIORITY: FR 1986-401380 19860623
DOCUMENT TYPE: Utility; APPLICATION.

AB A variant of a LAV virus, designated LAV.sub.MAL and capable of causing AIDS. The cDNA and antigens of the LAV.sub.MAL virus can be used for the diagnosis of AIDS and pre-AIDS.

CLM What is claimed is:
1. The virus LAV.sub.MAL comprising RNA corresponding to the cDNA of FIGS. 7A-7I.

2. The cDNA of FIGS. 7A-7I.

3. A DNA recombinant comprising the cDNA of claim 2.

4. A probe containing a nucleic acid sequence hybridizable with RNA of said LAV.sub.MAL virus of claim 1.

5. A method for identifying the presence in a host tissue of LAV virus which comprises hybridizing RNA obtained from said tissue with said probe of claim 4.

6. The method of claim 5, wherein said probe can hybridize with RNA from said LAV.sub.MAL virus to identify said LAV.sub.MAL virus.

7. A peptide or fragment thereof whose amino acid sequence is encoded by an open reading frame of a cDNA sequence of the LAV.sub.MAL virus of claim 1.

8. The peptide of claim 7 encoded by a cDNA sequence from amino-acyl residue 37 to amino-acyl residue 130, or from amino-acyl residue 211 to amino-acyl residue 289, or from amino-acyl residue 488 to amino-acyl residue 530 of FIGS. 3A-3F and 7A-7I.

9. The peptide of claim 7 encoded by a cDNA sequence from amino-acyl residue 490 to amino-acyl residue 620 or from amino-acyl residue 680 to amino-acyl residue 700 of FIGS. 3A-3F and 7A-7I.

10. The peptide of claim 7 which comprises a protein or glycoprotein whose amino acid sequence is encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: OMP or gp110 proteins, including precursors: 1 to 530; OMP or gp110 without precursor: 34-530; and TMP or gp41 protein: 531-877.

11. The peptide of claim 10 encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: 37-130, 211-289, 488-530, 490-620 or 680-700.

12. A method for the in vitro detection of the presence of an antibody directed against a LAV virus in a human body fluid, which comprises: contacting said body fluid with an antigen obtained from said virus

LAV.sub.MAL of claim 1, said antigen consisting of a peptide or a fragment thereof whose amino acid sequence is encoded by an open reading frame of a cDNA sequence of FIGS. 7A-7I; and then detecting the immunological reaction between said antigen and said antibody.

13. The method of claim 12 wherein said antigen detects said LAV.sub.MAL virus of claim 1.

14. The method of claim 12 which comprises the steps of: a) depositing a predetermined amount of said antigen into a cup of a titration microplate; b) introducing increasing dilutions of said body fluid into said cup; c) incubating said microplate; d) washing the microplate with a buffer; e) adding into said cup a labelled antibody directed against blood immunoglobulins; and then f) determining whether an antigen-antibody-complex has formed in said cup which is indicative of the presence of a LAV antibody in said body fluid.

15. A diagnostic kit for the in vitro detection of antibodies against a LAV virus, which kit comprises: an antigen consisting of a peptide of claim 7.

16. The kit of claim 15 wherein the antigen consists of a peptide of said LAV.sub.MAL virus of claim 1, encoded by the open reading frame of a cDNA sequence of said LAV.sub.MAL virus.

17. An immunogenic composition comprising: an antigen of the LAV.sub.MAL virus of claim 1 or an immunogenic peptide or fragment thereof encoded by RNA of said virus; and a physiologically acceptable carrier.

18. The immunogenic composition of claim 17 wherein said peptide is the gp110 envelope glycoprotein or a fragment thereof.

19. The immunogenic composition of claim 17 wherein the peptide comprises a protein or glycoprotein hwose amino acid sequence is encoded by all or part of one of the following cDNA sequences of FIGS. 3a-3F and 7A-7I: OMP or gp110 proteins, including precursors: 1 to 530; OMP or gp110 without precursor: 34-530; and TMP or gp41:531-877.

20. The composition of claim 19 wherein the protein or glycoprotein is encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: 37-130, 211-289, 488-530, 490-620 or 680-700.

21. An antibody formed against a peptide of claim 7.

22. A cell transformed with a DNA recombinant of claim 3.

L4 ANSWER 2 OF 13 USPATFULL
2002:301085 Variant of LAV viruses.
Alizon, Marc, Paris, FRANCE
Sonigo, Pierre, Paris, FRANCE
Wain-Hobson, Simon, Montigny Les Bretonneux, FRANCE
Montagnier, Luc, Le Plessis Robinson, FRANCE
Institut Pasteur of Paris (non-U.S. corporation)
US 2002168628 A1 20021114
APPLICATION: US 2001-17580 A1 20011218 (10)
PRIORITY: EP 1986-401380 19860623
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A variant of a LAV virus, designated LAV.sub.MAL and capable of causing

AIDS. The cDNA and antigens of the LAV.sub.MAL virus can be used for the diagnosis of AIDS and pre-AIDS.

CLM What is claimed is:

1. The virus LAV.sub.MAL comprising RNA corresponding to the cDNA of FIGS. 7A-7I.

2. The cDNA of FIGS. 7A-7I.

3. A DNA recombinant comprising the cDNA of claim 2.

4. A probe containing a nucleic acid sequence hybridizable with RNA of said LAV.sub.MAL virus of claim 1.

5. A method for identifying the presence in a host tissue of LAV virus which comprises hybridizing RNA obtained from said tissue with said probe of claim 4.

6. The method of claim 5, wherein said probe can hybridize with RNA from said LAV.sub.MAL virus to identify said LAV.sub.MAL virus.

7. A peptide or fragment thereof whose amino acid sequence is encoded by an open reading frame of a cDNA sequence of the LAV.sub.MAL virus of claim 1.

8. The peptide of claim 7 encoded by a cDNA sequence from amino-acyl residue 37 to amino-acyl residue 130, or from amino-acyl residue 211 to amino-acyl residue 289, or from amino-acyl residue 488 to amino-acyl residue 530 of FIGS. 3A-3F and 7A-7I.

9. The peptide of claim 7 encoded by a cDNA sequence from amino-acyl residue 490 to amino-acyl residue 620 or from amino-acyl residue 680 to amino-acyl residue 700 of FIGS. 3A-3F and 7A-7I.

10. The peptide of claim 7 which comprises a protein or glycoprotein whose amino acid sequence is encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: OMP or gp110 proteins, including precursors: 1 to 530; OMP or gp110 without precursor: 34-530; and TMP or gp41 protein: 531-877.

11. The peptide of claim 10 encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: 37-130, 211-289, 488-530, 490-520 or 680-700.

12. A method for the in vitro detection of the presence of an antibody directed against a LAV virus in a human body fluid, which comprises: contacting said body fluid with an antigen obtained from said virus LAV.sub.MAL of claim 1, said antigen consisting of a peptide or a fragment thereof whose amino acid sequence is encoded by an open reading frame of a cDNA sequence of FIGS. 7A-7I; and then detecting the immunological reaction between said antigen and said antibody.

13. The method of claim 12 wherein said antigen detects said LAV.sub.MAL virus of claim 1.

14. The method of claim 12 which comprises the steps of: a) depositing a predetermined amount of said antigen into a cup of a titration microplate; b) introducing increasing dilutions of said body fluid into said cup; c) incubating said microplate; d) washing the microplate with a buffer; e) adding into said cup a labelled antibody directed against blood immunoglobulins; and then f) determining whether an

antigen-antibody-complex has formed in said cup which is indicative of the presence of a LAV antibody in said body fluid.

15. A diagnostic kit for the in vitro detection of antibodies against a LAV virus, which kit comprises: an antigen consisting of a peptide of claim 7.

16. The kit of claim 15 wherein the antigen consists of a pepti.de of said LAV.sub.MAL virus of claim 1, encoded by the open reading frame of a cDNA sequence of said LAV.sub.MAL virus.

17. An immunogenic composition comprising: an antigen of the LAV.sub.MAL virus of claim 1 or an immunogenic peptide or fragment thereof encoded by RNA of said virus; and a physiologically acceptable carrier.

18. The immunogenic composition of claim 17 wherein said peptide is the gp110 envelope glycoprotein or a fragment thereof.

19. The immunogenic composition of claim 17 wherein the peptide comprises a protein or glycoprotein hwose amino acid sequence is encoded by all or part of one of the following cDNA sequences of FIGS. 3a-3F and 7A-7I: OMP or gp110 proteins, including precursors: 1 to 530; OMP or gp110 without precursor: 34-530; and TMP or gp41: 531-877.

20. The composition of claim 19 wherein the protein or glycoprotein is encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: 37-130, 211-289, 488-530, 490-620 or 680-700.

21. An antibody formed against a peptide of claim 7.

22. A cell transformed with a DNA recombinant of claim 3.

L4 ANSWER 3 OF 13 USPATFULL
2002:217017 Nucleic acids and peptides of human immunodeficiency virus type (HIV-1).
Montangnier, Luc, Le Plessis Robinson, FRANCE
Krust, Bernard, Paris, FRANCE
Chamaret, Solange, Paris, FRANCE
Clavel, Fran.cedilla.ois, Paris, FRANCE
Chermann, Jean-Claude, Elancourt, FRANCE
Barre-Sinoussi, Fran.cedilla.oise, Issy les Moulineaux, FRANCE
Alizon, Marc, Paris, FRANCE
Sonigo, Pierre, Paris, FRANCE
Cole, Stewart, Chatillon, FRANCE
Danos, Olivier, Paris, FRANCE
Wain-Hobson, Simon, Montigny les Bretonneux, FRANCE
Institut Pasteur, Paris, FRANCE (non-U.S. corporation)Centre National de la Recherche Scientifique, Paris, FRANCE (non-U.S. corporation)
US 6440657 B1 20020827
APPLICATION: US 2000-478492 20000106 (9)
PRIORITY: GB 1984-29099 19841116
CA 1985-493377 19851018
DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The molecular cloning and characterization of a novel human retrovirus, designated lymphadenopathy-associated virus, or LAV, is disclosed. LAV was originally isolated from a patient with acquired immune deficiency syndrome (AIDS). A cloned LAV complementary DNA (cDNA) was used to screen a library of recombinant phages constructed from the genomic DNA

of LAV-infected T lymphocytes. The nucleotide sequence of an insert obtained from the recombinant phage clone .lambda.J19 was ascertained through M13 shotgun cloning and the dideoxy chain termination sequencing method. The env coding region was identified and various hydrophilic peptides obtained therefrom. These peptides correspond to amino acids 551-577, 594-603, 621-630, 657-679, and 719-758 of the LAV envelope glycoprotein. These peptides should provide suitable diagnostic reagents for the detection LAV-specific antibodies and for the generation of LAV-specific immunological reagents.

CLM What is claimed is:

1. A chemically synthesized env peptide of Human Immunodeficiency Virus (HIV) of less than 150 amino acid residues, wherein the peptide comprises the sequence: Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu.

2. A chemically synthesized env peptide of Human Immunodeficiency Virus (HIV) of less than 150 amino acid residues, wherein the peptide comprises the sequence: Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln.

3. A chemically synthesized env peptide of Human Immunodeficiency Virus (HIV) of less than 150 amino acid residues, wherein the peptide comprises the sequence: Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser.

4. A chemically synthesized env peptide of Human Immunodeficiency Virus (HIV) of less than 150 amino acid residues, wherein the peptide comprises the sequence: Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala.

5. A chemically synthesized env peptide of Human Immunodeficiency Virus (HIV) of less than 150 amino acid residues, wherein the peptide comprises the sequence: Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile.

6. An in vitro diagnostic method for the detection of the presence or absence of antibodies that bind to antigens of HIV-1 retrovirus comprising: (a) contacting at least one peptide of any one of claims 1 to 5 with a biological fluid for a time and under conditions sufficient for said peptide and antibody in the biological fluid to form a peptide-antibody complex; (b) detecting the formation of the peptide-antibody complex by comparing said formation of the peptide-antibody complex with a control sample, wherein the formation of the peptide-antibody complex is correlated with the presence of antibodies that bind to antigens of HIV-1 retrovirus in said biological sample.

L4 ANSWER 4 OF 13 USPATFULL
2002:188123 Variant of LAV viruses.
Alizon, Marc, Paris, FRANCE
Sonigo, Pierre, Paris, FRANCE
Wain-Hobson, Simon, Montigny les Bretonneux, FRANCE
Montagnier, Luc, Le Plessis Robinson, FRANCE
Institut Pasteur, FRANCE (non-U.S. corporation)
US 6426073 B1 20020730
APPLICATION: US 1999-328438 19990609 (9)
PRIORITY: FR 1986-401380 19860623

DOCUMENT TYPE: Utility; GRANTED.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to a novel human immunodeficiency virus (HIV) capable of inducing lymphadenopathies (LAS) and acquired immune deficiency syndromes (AIDS) in patients which has been designated the lymphadenopathy associated virus strain MAL (LAV.sub.MAL). Although the overall genomic organization of LAV.sub.MAL is similar to other known HIV-1 isolates such as LAV.sub.BRU and HTLV-III, nevertheless, this virus also displays considerable genotypic and phenotypic diversity as compared to these isolates. A proviral molecular clone of the virus was obtained and characterized. The complete nucleotide sequence of this clone was ascertained and putative regulatory regions (e.g., U3, R, U5,), regulatory elements (e.g., the TATA box, AATAAA polyadenylation signal, primer binding site), and open reading frames (e.g., Gag, Pol, Env, Vif, Vpr, Tat, Rev, Nef) identified. Of particular interest are unique polypeptides derived from the viral envelope. The claimed invention is directed toward isolated LAV.sub.MAL Env polypeptides consisting of 5-150 amino acids wherein said peptides contain a LAV.sub.MAL-specific epitope. These peptides will prove useful, inter alia, as diagnostic reagents and in the generation of immunological reagents for the detection of the virus.

CLM What is claimed is:
1. An isolated HIV-1 LAV.sub.MAL Env polypeptide consisting of 5-150 amino acid residues as set forth in FIGS. 3E-3F, wherein said peptide contains a LAV.sub.MAL-specific antigenic determinant.

2. The peptide of claim 1, wherein said peptide is generated by chemical cleavage.

3. The peptide of claim 1, wherein said peptide is expressed from a recombinant DNA.

4. The peptide of claim 1, wherein said peptide is generated by chemical synthesis.

5. The peptide of claim 1, wherein said peptide binds to antibodies in AIDS patient sera; and wherein said antibodies are capable of binding to viral antigens encoded by the LAV.sub.MAL molecular clone having C.N.C.M. accession number I-641.

L4 ANSWER 5 OF 13 USPATFULL
2002:164667 Variant of LAV viruses.
Alizon, Marc, Paris, FRANCE
Sonigo, Pierre, Paris, FRANCE
Wain-Hobson, Simon, Montigny Les Bretonneux, FRANCE
Montagnier, Luc, Le Plessis Robinson, FRANCE
Institut Pasteur, Paris, FRANCE (non-U.S. corporation)
US 2002086285 A1 20020704
APPLICATION: US 2001-986799 A1 20011113 (9)
PRIORITY: EP 1986-401380 19860623
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A variant of a LAV virus, designated LAV.sub.ELI and capable of causing AIDS. The cDNA and antigens of the LAV.sub.ELI virus can be used for the diagnosis of AIDS and pre-AIDS.

CLM What is claimed is:

1. The virus LAV.sub.ELI comprising RNA corresponding to the CDNA of FIGS. 7A-7I.

2. The cDNA of FIGS. 7A-7I.

3. A DNA recombinant comprising the CDNA of claim 2.

4. A probe containing a nucleic acid sequence hybridizable with RNA of said LAV.sub.ELI virus of claim 1.

5. A method for identifying the presence in a host tissue of LAV virus which comprises hybridizing RNA obtained from said tissue with said probe of claim 4.

6. The method of claim 5, wherein said probe can hybridize with RNA from said LAV.sub.ELI virus to identify said LAV.sub.ELI virus.

7. A peptide or fragment thereof whose amino acid sequence is encoded by an open reading frame of a cDNA sequence of the LAV.sub.ELI virus of claim 1.

8. The peptide of claim 7 encoded by a cDNA sequence from amino-acyl residue 37 to amino-acyl residue 130, or from amino-acyl residue 211 to amino-acyl residue 289, or from amino-acyl residue 488 to amino-acyl residue 530 of FIGS. 3A-3F and 7A-71.

9. The peptide of claim 7 encoded by a cDNA sequence from amino-acyl residue 490 to amino-acyl residue 620 or from amino-acyl residue 680 to amino-acyl residue 700 of FIGS. 3A-3F and 7A-7I.

10. The peptide of claim 7 which comprises a protein or glycoprotein whose amino acid sequence is encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: OMP or gp110 proteins, including precursors: 1 to 530; OMP or gp110 without precursor: 34-530; and TMP or gp41 protein: 531-877.

11. The peptide of claim 10 encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: 37-130, 211-289, 488-530, 490-620 or 680-700.

12. A method for the in vitro detection of the presence of an antibody directed against a LAV virus in a human body fluid, which comprises: contacting said body fluid with an antigen obtained from said virus LAV.sub.ELI of claim 1, said antigen consisting of a peptide or a fragment thereof whose amino acid sequence is encoded by an open reading frame of a cDNA sequence of FIGS. 7A-7I; and then detecting the immunological reaction between said antigen and said antibody.

13. The method of claim 12 wherein said antigen detects said LAV.sub.ELI virus of claim 1.

14. The method of claim 12 which comprises the steps of: a) depositing a predetermined amount of said antigen into a cup of a titration microplate; b) introducing increasing dilutions of said body fluid into said cup; c) incubating said microplate; d) washing the microplate with a buffer; e) adding into said cup a labelled antibody directed against blood immunoglobulins; and then f) determining whether an antigen-antibody-complex has formed in said cup which is indicative of the presence of a LAV antibody in said body fluid.

15. A diagnostic kit for the in vitro detection of antibodies against a

LAV virus, which kit comprises: an antigen consisting of a peptide of claim 7.

16. The kit of claim 15 wherein the antigen consists of a peptide of said LAV.sub.ELI virus of claim 1, encoded by an open reading frame of a cDNA sequence of said LAV.sub.ELI virus.

17. An immunogenic composition comprising: an antigen of the LAV.sub.ELI virus of claim 1 or an immunogenic peptide or fragment thereof encoded by RNA of said virus; and a physiologically acceptable carrier.

18. The immunogenic composition of claim 17 wherein said peptide is the gp110 envelope glycoprotein or a fragment thereof.

19. The immunogenic composition of claim 17 wherein the peptide comprises a protein or glycoproteln whose amino acid sequence is encoded by all or part of one of the following cDNA sequences of FIGS. 3a-3F and 7A-7I: OMP or gp110 proteins, including precursors: 1 to 530; OMP or gp110 without precursor: 34-530; and TMP or gp41: 531-877.

20. The composition of claim 19 wherein the protein or glycoprotein is encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-71: 37-130, 211-289, 488-530, 490-620 or 680-700.

21. An antibody formed against a peptide of claim 7.

22. A cell transformed with a DNA recombinant of claim 3.

L4 ANSWER 6 OF 13 USPATFULL
2002:148551 Variant of LAV viruses.
Alizon, Marc, Paris, FRANCE
Sonigo, Pierre, Paris, FRANCE
Wain-Hobson, Simon, Montigny Les Bretonneux, FRANCE
Montagnier, Luc, Le Plessis Robinson, FRANCE
Institut Pasteur, Paris, FRANCE (non-U.S. corporation)
US 2002076691 A1 20020620
APPLICATION: US 2001-767138 A1 20010123 (9)
PRIORITY: EP 1986-401380 19860623
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A variant of a LAV virus, designated LAV.sub.ELI and capable of causing AIDS. The cDNA and antigens of the LAV.sub.ELI virus can be used for the diagnosis of AIDS and pre-AIDS.

CLM What is claimed is:
1. The virus LAV.sub.ELI comprising RNA corresponding to the cDNA of FIGS. 7A-7I.

2. The cDNA of FIGS. 7A-7I.

3. A DNA recombinant comprising the cDNA of claim 2.

4. A probe containing a nucleic acid sequence hybridizable with RNA of said LAV.sub.ELI virus of claim 1.

5. A method for identifying the presence in a host tissue of LAV virus which comprises hybridizing RNA obtained from said tissue with said probe of claim 4.

6. The method of claim 5, wherein said probe can hybridize with RNA from said LAV.sub.ELI virus to identify said LAV.sub.ELI virus.

7. A peptide or fragment thereof whose amino acid sequence is encoded by an open reading frame of a cDNA sequence of the LAV.sub.ELI virus of claim 1.

8. The peptide of claim 7 encoded by a cDNA sequence from amino-acyl residue 37 to amino-acyl residue 130, or from amino-acyl residue 211 to amino-acyl residue 289, or from amino-acyl residue 488 to amino-acyl residue 530 of FIGS. 3A-3F and 7A-7I.

9. The peptide of claim 7 encoded by a cDNA sequence from amino-acyl residue 490 to amino-acyl residue 620 or from amino-acyl residue 680 to amino-acyl residue 700 of FIGS. 3A-3F and 7A-7I.

10. The peptide of claim 7 which comprises a protein or glycoprotein whose amino acid sequence is encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: OMP or gp110 proteins, including precursors: 1 to 530; OMP or gp110 without precursor: 34-530; and TMP or gp41 protein: 531-877.

11. The peptide of claim 10 encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: 37-130, 211-289, 488-530, 490-620 or 680-700.

12. A method for the in vitro detection of the presence of an antibody directed against a LAV virus in a human body fluid, which comprises: contacting said body fluid with an antigen obtained from said virus LAV.sub.ELI of claim 1, said antigen consisting of a peptide or a fragment thereof whose amino acid sequence is encoded by an open reading frame of a cDNA sequence of FIGS. 7A-7I; and then detecting the immunological reaction between said antigen and said antibody.

13. The method of claim 12 wherein said antigen detects said LAV.sub.ELI virus of claim 1.

14. The method of claim 12 which comprises the steps of: a) depositing a predetermined amount of said antigen into a cup of a titration microplate; b) introducing increasing dilutions of said body fluid into said cup; c) incubating said microplate; d) washing the microplate with a buffer; e) adding into said cup a labelled antibody directed against blood immunoglobulins; and then f) determining whether an antigen-antibody-complex has formed in said cup which is indicative of the presence of a LAV antibody in said body fluid.

15. A diagnostic kit for the in vitro detection of antibodies against a LAV virus, which kit comprises: an antigen consisting of a peptide of claim 7.

16. The kit of claim 15 wherein the antigen consists of a peptide of said LAV.sub.ELI virus of claim 1, encoded by an open reading frame of a cDNA sequence of said LAV.sub.ELI virus.

17. An immunogenic composition comprising: an antigen of the LAV.sub.ELI virus of claim 1 or an immunogenic peptide or fragment thereof encoded by RNA of said virus; and a physiologically acceptable carrier.

18. The immunogenic composition of claim 17 wherein said peptide is the gp110 envelope glycoprotein or a fragment thereof.

19. The immunogenic composition of claim 17 wherein the peptide comprises a protein or glycoprotein whose amino acid sequence is encoded by all or part of one of the following cDNA sequences of FIGS. 3a-3F and 7A-7I: OMP or gp110 proteins, including precursors: 1 to 530; OMP or gp110 without precursor: 34-530; and TMP or gp41: 531-877.

20. The composition of claim 19 wherein the protein or glycoprotein is encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: 37-130, 211-289, 488-530, 490-620 or 680-700.

21. An antibody formed against a peptide of claim 7.

22. A cell transformed with a DNA recombinant of claim 3.

L4 ANSWER 7 OF 13 USPATFULL
2002:37317 Variant of LAV viruses.
Alizon, Marc, Paris, FRANCE
Sonigo, Pierre, Paris, FRANCE
Wain-Hobson, Simon, Montigny Les Bretonneux, FRANCE
Montagnier, Luc, Le Plessis Robinson, FRANCE
Institut Pasteur (non-U.S. corporation)
US 2002022033 A1 20020221
APPLICATION: US 2001-834627 A1 20010416 (9)
PRIORITY: EP 1986-401380 19860623
DOCUMENT TYPE: Utility; APPLICATION.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A variant of a LAV virus, designated LAV.sub.MAL and capable of causing AIDS. The cDNA and antigens of the LAV.sub.MAL virus can be used for the diagnosis of AIDS and pre-AIDS.

CLM What is claimed is:
1. The virus LAV.sub.MAL comprising RNA corresponding to the cDNA of FIGS. 7A-7I.

2. The CDNA of FIGS. 7A-7I.

3. A DNA recombinant comprising the cDNA of claim 2.

4. A probe containing a nucleic acid sequence hybridizable with RNA of said LAV.sub.MAL virus of claim 1.

5. A method for identifying the presence in a host tissue of LAV virus which comprises hybridizing RNA obtained from said tissue with said probe of claim 4.

6. The method of claim 5, wherein said probe can hybridize with RNA from said LAV.sub.MAL virus to identify said LAV.sub.MAL virus.

7. A peptide or fragment thereof whose amino acid sequence is encoded by an open reading frame of a cDNA sequence of the LAV.sub.MAL virus of claim 1.

8. The peptide of claim 7 encoded by a cDNA sequence from amino-acyl residue 37 to amino-acyl residue 130, or from amino-acyl residue 211 to amino-acyl residue 289, or from amino-acyl residue 488 to amino-acyl residue 530 of FIGS. 3A-3F and 7A-7I.

9. The peptide of claim 7 encoded by a cDNA sequence from amino-acyl residue 490 to amino-acyl residue 620 or from amino-acyl residue 680 to

amino-acyl residue 700 of FIGS. 3A-3F and 7A-7I.

10. The peptide of claim 7 which comprises a protein or glycoprotein whose amino acid sequence is encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: OMP or gp110 proteins, including precursors: 1 to 530; OMP or gp110 without precursor: 34-530; and TMP or gp41 protein: 531-877.

11. The peptide of claim 10 encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: 37-130, 211-289, 488-530, 490-620 or 680-700.

12. A method for the in vitro detection of the presence of an antibody directed against a LAV virus in a human body fluid, which comprises: contacting said body fluid with an antigen obtained from said virus LAV.sub.MAL of claim 1, said antigen consisting of a peptide or a fragment thereof whose amino acid sequence is encoded by an open reading frame of a cDNA sequence of FIGS. 7A-7I; and then detecting the immunological reaction between said antigen and said antibody.

13. The method of claim 12 wherein said antigen detects said LAV.sub.MAL virus of claim 1.

14. The method of claim 12 which comprises the steps of: a) depositing a predetermined amount of said antigen into a cup of a titration microplate; b) introducing increasing dilutions of said body fluid into said cup; c) incubating said microplate; d) washing the microplate with a buffer; e) adding into said cup a labelled antibody directed against blood immunoglobulins; and then f) determining whether an antigen-antibody-complex has formed in said cup which is indicative of the presence of a LAV antibody in said body fluid.

15. A diagnostic kit for the in vitro detection of antibodies against a LAV virus, which kit comprises: an antigen consisting of a peptide of claim 7.

16. The kit of claim 15 wherein the antigen consists of a peptide of said LAV.sub.MAL virus of claim 1, encoded by the open reading frame of a cDNA sequence of said LAV.sub.MAL virus.

17. An immunogenic composition comprising: an antigen of the LAV.sub.MAL virus of claim 1 or an immunogenic peptide or fragment thereof encoded by RNA of said virus; and a physiologically acceptable carrier.

18. The immunogenic composition of claim 17 wherein said peptide is the gp110 envelope glycoprotein or a fragment thereof.

19. The immunogenic composition of claim 17 wherein the peptide comprises a protein or glycoprotein hwose amino acid sequence is encoded by all or part of one of the following cDNA sequences of FIGS. 3a-3F and 7A-7I: OMP or gp110 proteins, including precursors: 1 to 530; OMP or gp110 without precursor: 34-530; and TMP or gp41: 531-877.

20. The composition of claim 19 wherein the protein or glycoprotein is encoded by all or part of one of the following cDNA sequences of FIGS. 3A-3F and 7A-7I: 37-130, 211-289, 488-530, 490-620 or 680-700.

21. An antibody formed against a peptide of claim 7.

22. A cell transformed with a DNA recombinant of claim 3.

L4 ANSWER 8 OF 13 USPATFULL
1999:141307 Amino acid DNA sequences related to genomic RNA of human immunodeficiency virus (HIV-1).
Alizon, Marc, Paris, France
Sonigo, Pierre, Paris, France
Stewart, Cole, Chatillon, France
Danos, Oliver, Paris, France
Wain-Hobson, Simon, Montigny Les Bretonneux, France
Institut Pasteur and Centre National de la Recherche Scientifique, Paris, France (non-U.S. corporation)
US 5980900 19991109
APPLICATION: US 1991-751059 19910828 (7)
PRIORITY: FR 1984-16013 19841018
GB 1984-29099 19841116
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB This invention is in the field of lymphadenopathy virus which has been desogmated Human Immunodeficiency Virus Type 1 (HIV-1) This invention relates to a diagnostic means and method to detect the presence of DNA, RNA or antibodies of the lymphadenopathy retrovirus associated with the acquired immune deficiency syndrome or of the lymphadenopathy syndrome by the use of DNA fragments or the peptides encoded by said DNA fragments. The invention further relates to the DNA fragments, vectors comprising them and the proteins expressed.

CLM What is claimed is:
1. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acid 8 to 23 of the env gene, where in the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Met-Arg-Val-Lys-Glu-Lys-Tyr-Gln-His-Leu-Trp-Arg-Trp-Gly-Trp-Lys-.

2. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 63 to 78 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Ser-Asp-Ala-Lys-Ala-Tyr-Asp-Thr-Glu-Val-His-Asn-Val-Trp-Ala-Thr-.

3. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 82 to 90 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Val-Pro-Thr-Asp-Pro-Asn-Pro-Gln-Glu-.

4. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 97 to 123 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Thr-Glu-Asn-Phe-Asn-Met-Trp-Lys-Asn-Asp-Met-Val-Glu-Gln-Met-His-Glu-Asp-Ile-Ile-Ser-Leu-Trp-Asp-Gln-Ser-Leu-.

5. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 127 to 183 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Val-Lys-Leu-Thr-Pro-Leu-Cys-Val-Ser-Leu-Lys-Cys-Thr-Asp-Leu-Gly-Asn-Ala-Thr-Asn-Thr-Asn-Ser-Ser-Asn-Thr-Asn-Ser-Ser-Ser-Gly-Glu-Met-Met-Met-Glu-Lys-Gly-Glu-Ile-Lys-Asn-Cys-Ser-Phe-Asn-Ile-Ser-Thr-Ser-Ile-Arg-Gly-Lys-Val-Gln-Lys-.

6. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 197 to 201 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Leu-Asp-Ile-Ile-Pro-Ile-Asp-Asn-Asp-Thr-Thr-.

7. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 239 to 294 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Lys-Cys-Asn-Asn-Lys-Thr-Phe-Asn-Gly-Thr-Gly-Pro-Cys-Thr-Asn-Val-Ser-Thr-Val-Gln-Cys-Thr-His-Gly-Ile-Arg-Pro-Val-Val-Ser-Thr-Gln-Leu-Leu-Leu-Asn-Gly-Ser-Leu-Ala-Glu-Glu-Glu-Val-Val-Ile-Arg-Ser-Ala-Asn-Phe-Thr-Asp-Asn-Ala-Lys-.

8. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 300 to 327 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Leu-Asn-Gln-Ser-Val-Glu-Ile-Asn-Cys-Thr-Arg-Pro-Asn-Asn-Asn-Thr-Arg-Lys-Ser-Ile-Arg-Ile-Gln-Arg-Gly-Pro-Gly-Arg-.

9. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 334 to 381 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Lys-Ile-Gly-Asn-Met-Arg-Gln-Ala-His-Cys-Asn-Ile-Ser-Arg-Ala-Lys-Trp-Asn-Ala-Thr-Leu-Lys-Gln-Ile-Ala-Ser-Lys-Leu-Arg-Glu-Gln-Phe-Gly-Asn-Asn-Lys-Thr-Ile-Ile-Phe-Lys-Gln-Ser-Ser-Gly-Gly-Asp-Pro-.

10. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 397 to 424 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Cys-Asn-Ser-Thr-Gln-Leu-Phe-Asn-Ser-Thr-Trp-Phe-Asn-Ser-Thr-Trp-Ser-Thr-Glu-Gly-Ser-Asn-Asn-Thr-Glu-Gly-Ser-Asp-.

11. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 466 to 500 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Leu-Thr-Arg-Asp-Gly-Gly-Asn-Asn-Asn-Asn-Gly-Ser-Glu-Ile-Phe-Arg-Pro-Gly-Gly-Gly-Asp-Met-Arg-Asp-Asn-Trp-Arg-Ser-Glu-Leu-Tyr-Lys-Tyr-Lys-Val-.

12. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 510 to 523 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Pro-Thr-Lys-Ala-Lys-Arg-Arg-Val-Val-Gln-Arg-Glu-Lys-Arg-.

13. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 551 to 577 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Val-Gln-Ala-Arg-Gln-Leu-Leu-Ser-Gly-Ile-Val-Gln-Gln-Gln-Asn-Asn-Leu-Leu-Arg-Ala-Ile-Glu-Ala-Gln-Gln-His-Leu-.

14. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 594 to 603 of the env gene, wherein the amino acid sequence is free of particles

of said virus and the amino acid sequence comprises the following: Ala-Val-Glu-Arg-Tyr-Leu-Lys-Asp-Gln-Gln-.

15. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 621 to 630 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Pro-Trp-Asn-Ala-Ser-Trp-Ser-Asn-Lys-Ser-.

16. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 657 to 679 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Leu-Ile-Glu-Glu-Ser-Gln-Asn-Gln-Gln-Glu-Lys-Asn-Glu-Gln-Glu-Leu-Leu-Glu-Leu-Asp-Lys-Trp-Ala-.

17. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 719 to 758 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Arg-Val-Arg-Gln-Gly-Tyr-Ser-Pro-Leu-Ser-Phe-Gln-Thr-His-Leu-Pro-Thr-Pro-Arg-Gly-Pro-Asp-Arg-Pro-Glu-Gly-Ile-Glu-Glu-Glu-Gly-Gly-Glu-Arg-Asp-Arg-Asp-Arg-Ser-Ile-.

18. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), consisting essentially of amino acids 780 to 803 of the env gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Tyr-His-Arg-Leu-Arg-Asp-Leu-Leu-Leu-Ile-Val-Thr-Arg-Ile-Val-Glu-Leu-Leu-Gly-Arg-Arg-Gly-Trp-Glu-.

19. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 6096 to about 6200; and the amino acid sequence consists essentially of the following: Asn-Ala-Thr-Asn-Thr-Asn-Ser-Ser-Asn-Thr-Asn-Ser-Ser-Ser-Gly-Glu-Met-Met-Met-Glu-Lys-Gly-Glu-Ile-Lys-Asn-Cys-Ser-Phe-Asn-Ile-Ser-Thr-Ser-Ile.

20. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 6261 to about 6311; and the amino acid sequence consists essentially of the following: Asn-Asp-Thr-Thr-Ser-Tyr-Thr-Leu-Thr-Ser-Cys-Asn-Thr-Ser-Val-Ile-Thr.

21. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 6390 to about 6440; and the amino acid sequence consists essentially of the following: Asn-Asn-Lys-Thr-Phe-Asn-Gly-Thr-Gly-Pro-Cys-Thr-Asn-Val-Ser-Thr-Val.

22. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 6486 to about 6620; and the amino acid sequence consists essentially of the following: Leu-Asn-Gly-Ser-Leu-Ala-Glu-Glu-Glu-Val-Val-Ile-Arg-Ser-Ala-Asn-Phe-Thr-Asp-Asn-Ala-Lys-Thr-Ile-Ile-Val-Gln-Leu-Asn-Gln-Ser-Val-Glu-Ile-Asn-Cys-Thr-Arg-Pro-Asn-Asn-Asn-Thr-Arg-Lys.

23. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 6861 to about 6929; and the amino acid sequence consists essentially of the following: Asn-Ser-Thr-Gln-Leu-Phe-Asn-Ser-Thr-Trp-Phe-Asn-Ser-Thr-Trp-Ser-Thr-Glu-Gly-Ser-Asn-Leu-Thr.

24. An amino acid sequence of Human Immunodeficiency Virus Type 1 (HIV-1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 7536 to about 7631; and the amino acid sequence consists essentially of the following: Asn-Ala-Ser-Trp-Ser-Asn-Lys-Ser-Leu-Glu-Gln-Ile-Trp-Asn-Asn-Met-Thr-Trp-Met-Glu-Trp-Asp-Arg-Glu-Ile-Asn-Asn-Tyr-Thr-Ser-Leu-Ile.

25. An immunogenic composition comprising one or more peptides according to any one of claims 1 to 24.

26. A composition consisting essentially of at least one of the amino acid sequences of Human Immunodeficiency Virus Type 1 (HIV-1) selected from the group consisting of: (1) the amino acid sequence encoded by the nucleotide sequence of the env gene of HIV-1 extending from about nucleotide 6095 to about nucleotide 6200; (2) the amino acid sequence encoded by the nucleotide sequence of the env gene of HIV-1 extending from about nucleotide 6260 to about nucleotide 6310; (3) the amino acid sequence encoded by the nucleotide sequence of the env gene of HIV-1 extending from about nucleotide 6390 to about nucleotide 6440; (4) the amino acid sequence encoded by the nucleotide sequence of the env gene of HIV-1 extending from about nucleotide 6485 to about nucleotide 6620; (5) the amino acid sequence encoded by the nucleotide sequence of the env gene of HIV-1 extending from about nucleotide 6860 to about nucleotide 6930; and (6) the amino acid sequence encoded by the nucleotide sequence of the env gene of HIV-1 extending from about nucleotide 7535 to about nucleotide 7630; wherein the amino acid sequences are free of particles of said virus.

27. An immunogenic composition comprising a peptide composition according to claim 26.

28. A composition consisting essentially of a mixture of two amino acid sequences of Human Immunodeficiency Virus Type 1 (HIV-1) selected from the group consisting of: (1) amino acids 8 to 23 of the env gene having the sequence Met-Arg-Val-Lys-Glu-Lys-Tyr-Gln-His-Leu-Trp-Arg-Trp-Gly-Trp-Lys-; (2) amino acids 63 to 78 of the env gene having the sequence Ser-Asp-Ala-Lys-Ala-Tyr-Asp-Thr-Glu-Val-His-Asn-Val-Trp-Ala-Thr-; (3) amino acids 82 to 90 of the env gene having the sequence Val-Pro-Thr-Asp-Pro-Asn-Pro-Gln-Glu-; (4) amino acids 97 to 123 of the env gene having the sequence Thr-Glu-Asn-Phe-Asn-Met-Trp-Lys-Asn-Asp-Met-Val-Glu-Gln-Met-His-Glu-Asp-Ile-Ile-Ser-Leu-Trp-Asp-Gln-Ser-Leu; (5) amino acids 127 to 183 of the env gene having the sequence Val-Lys-Leu-Thr-Pro-Leu-Cys-Val-Ser-Leu-Lys-Cys-Thr-Asp-Leu-Gly-Asn-Ala-Thr-Asn-Thr-Asn-Ser-Ser-Asn-Thr-Asn-Ser-Ser-Ser-Gly-Glu-Met-Met-Glu-Lys-Gly-Glu-Ile-Lys-Asn-Cys-Ser-Phe-Asn-Ile-Ser-Thr-Ser-Ile-Arg-Gly-Lys-Val-Gln-Lys-; (6) amino acids 197 to 201 of the env gene having the sequence Leu-Asp-Ile-Ile-Pro-Ile-Asp-Asn-Asp-Thr-Thr-; (7) amino acids 239 to 294 of the env gene having the sequence Lys-Cys-Asn-Asn-Lys-Thr-Phe-Asn-Gly-Thr-Gly-Pro-Cys-Thr-Asn-Val-Ser-Thr-Val-Gly-Cys-Thr-His-Gly-Ile-Arg-Pro-Val-Val-Ser-Thr-Gln-Leu-

Leu-Leu-Asn-Gly-Ser-Leu-Ala-Glu-Glu-Glu-Val-Val-Ile-Arg-Ser-Ala-Asn-Phe-Thr-Asp-Asn-Ala-Lys-; (8) amino acids 300 to 327 of the env gene having the sequence Leu-Asn-Gln-Ser-Val-Glu-Ile-Asn-Cys-Thr-Arg-Pro-Asn-Asn-Asn-Thr-Arg-Lys-Ser-Ile-Arg-Ile-Gln-Arg-Gly-Pro-Gly-Arg-; (9) amino acids 334 to 381 of the env gene having the sequence Lys-Ile-Gly-Asn-Met-Arg-Gln-Ala-His-Cys-Asn-Ile-Ser-Arg-Ala-Lys-Trp-Asn-Ala-Thr-Leu-Lys-Gln-Ile-Ala-Ser-Lys-Leu-Arg-Glu-Gln-Phe-Gly-Asn-Asn-Lys-Thr-Ile-Ile-Phe-Lys-Gln-Ser-Ser-Gly-Gly-Asp-Pro-; (10) amino acids 397 to 424 of the env gene having the sequence Cys-Asn-Ser-Thr-Gln-Leu-Phe-Asn-Ser-Thr-Trp-Phe-Asn-Ser-Thr-Trp-Ser-Thr-Glu-Gly-Ser-Asn-Asn-Thr-Glu-Gly-Ser-Asp-; (11) amino acids 466 to 500 of the env gene having the sequence Leu-Thr-Arg-Asp-Gly-Gly-Asn-Asn-Asn-Asn-Gly-Ser-Glu-Ile-Phe-Arg-Pro-Gly-Gly-Gly-Asp-Met-Arg-Asp-Asn-Trp-Arg-Ser-Glu-Leu-Tyr-Lys-Tyr-Lys-Val-; (12) amino acids 510 to 523 of the env gene having the sequence Pro-Thr-Lys-Ala-Lys-Arg-Arg-Val-Val-Gln-Arg-Glu-Lys-Arg-; (13) amino acids 551 to 577 of the env gene having the sequence Val-Gln-Ala-Arg-Gln-Leu-Leu-Ser-Gly-Ile-Val-Gln-Gln-Gln-Asn-Asn-Leu-Leu-Arg-Ala-Ile-Glu-Ala-Gln-Gln-His-Leu-; (14) amino acids 594 to 603 of the env gene having the sequence Ala-Val-Glu-Arg-Tyr-Leu-Lys-Asp-Gln-Gln-; (15) amino acids 621 to 630 of the env gene having the sequence Pro-Trp-Asn-Ala-Ser-Trp-Ser-Asn-Lys-Ser-; (16) amino acids 657 to 679 of the env gene having the sequence Leu-Ile-Glu-Glu-Ser-Gln-Asn-Gln-Gln-Glu-Lys-Asn-Glu-Gln-Glu-Leu-Leu-Glu-Leu-Asp-Lys-Trp-Ala-; (17) amino acids 719 to 758 of the env gene having the sequence Arg-Val-Arg-Gln-Gly-Tyr-Ser-Pro-Leu-Ser-Phe-Gln-Thr-His-Leu-Pro-Thr-Pro-Arg-Gly-Pro-Asp-Arg-Pro-Glu-Gly-Ile-Glu-Glu-Glu-Gly-Gly-Glu-Arg-Asp-Arg-Asp-Arg-Ser-Ile-; and (18) amino acid 780 to 803 of the env gene having the sequence Tyr-His-Arg-Leu-Arg-Asp-Leu-Leu-Leu-Ile-Val-Thr-Arg-Ile-Val-Glu-Leu-Leu-Gly-Arg-Arg-Gly-Trp-Glu-; wherein the amino acid sequences are free of particles of said virus.

29. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (1) and (2).

30. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (2) and (3).

31. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (3) and (4).

32. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (4) and (5).

33. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (5) and (6).

34. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (6) and (7).

35. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (7) and (8).

36. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (8) and (9).

37. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (9) and (10).

38. A composition as claimed in claim 28, wherein the composition

consists essentially of the amino acid sequences recited in (10) and (11).

39. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (11) and (12).

40. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (12) and (13).

41. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (13) and (14).

42. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (14) and (15).

43. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (15) and (16).

44. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (16) and (17).

45. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (17) and (18).

46. An immunogenic composition consisting essentially of a peptide composition according to claim 28.

47. An immunogenic composition comprising a peptide composition according to claim 30.

L4 ANSWER 9 OF 13 USPATFULL
1998:128076 Purification, cloning, and characterization of a novel human immunodeficiency virus LAV.sub.MAL.
Alizon, Marc, Paris, France
Sonigo, Pierre, Paris, France
Wain-Hobson, Simon, Montigney Les Bretonneux, France
Montagnier, Luc, Le Plessis Robinson, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5824482 19981020
APPLICATION: US 1995-471474 19950606 (8)
PRIORITY: FR 1986-40138 19860623
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB An HIV isolate, LAV.sub.MAL, has been purified, sequenced, and characterized at the genetic level. The entire nucleic acid sequence of the viral genome, the encoded amino acid sequences, and the open reading frames found in the genome are disclosed. Specific peptides relating to the envelope glycoprotein of the viral genome are discussed. These peptides can be used in diagnostic methods and kits for detecting the presence of an HIV virus.

CLM What is claimed is:
1. A purified virus, designated LAV.sub.MAL, having CNCM biological

deposit number I-641.

2. A method for the in vitro detection of the presence of an antibody directed against a LAV virus in a human body fluid, which comprises contacting said body fluid with an antigen obtained from a virus LAV.sub.MAL, said antigen selected from the group consisting of: a purified or synthetic peptide having an amino acid sequence of one of the open reading frames set forth in FIGS. 7A-7I; a purified or synthetic peptide having the amino acid sequence set forth as residues 37-130 of the envelope glycoprotein of LAV.sub.MAL ; a purified or synthetic peptide having the amino acid sequence set forth as residues 211-289 of the envelope glycoprotein of LAV.sub.MAL ; a purified or synthetic peptide having the amino acid sequence set forth as residues 488-530 of the envelope glycoprotein of LAV.sub.MAL ; a purified or synthetic peptide having the amino acid sequence set forth as residues 490-620 of the envelope glycoprotein of LAV.sub.MAL ; a purified or synthetic peptide having the amino acid sequence set forth as residues 680-700 of the envelope glycoprotein of LAV.sub.MAL ; purified or synthetic peptide having the amino acid sequence set forth as residues 1-530 of the envelope glycoprotein of LAV.sub.MAL ; a purified or synthetic peptide having the amino acid sequence set forth as residues 34-530 of the envelope glycoprotein of LAV.sub.MAL ; and a purified or synthetic peptide having the amino acid sequence set forth as residues 531-877 of the envelope glycoprotein of LAV.sub.MAL and detecting the immunological reaction between said antigen and said antibody.

3. The method of claim 2 comprising: (a) depositing a predetermined amount of said antigen into a cup of a titration microplate; (b) introducing increasing dilutions of said body fluid into said cup; (c) incubating said microplate; (d) washing the microplate with a buffer; (e) adding into said cup a labeled antibody directed against blood immunoglobulins; and then (f) determining whether an antigen-antibody-complex has formed in said cup which is indicative of the presence of a LAV antibody in said body fluid.

4. A diagnostic kit for the in vitro detection of antibodies against a LAV virus comprising (a) an antigen selected from the group consisting of: a purified or synthetic peptide (having the amino acid sequence of one of the open reading frames set forth in FIGS. 7A-7F; a purified or synthetic peptide having the amino acid sequence set forth as residues 37-130 of the envelope glycoprotein of LAV.sub.MAL ; a purified or synthetic peptide having the amino acid sequence set forth as residues 211-289 of the envelope glycoprotein of LAV.sub.MAL ; a purified or synthetic peptide having the amino acid sequence set forth as residues 488-530 of the envelope glycoprotein of LAV.sub.MAL ; a purified or synthetic peptide having the amino acid sequence set forth as residues 490-620 of the envelope glycoprotein of LAV.sub.MAL ; a purified or synthetic peptide having the amino acid sequence set forth as residues 680-700 of the envelope glycoprotein of LAV.sub.MAL ; a purified or synthetic peptide having the amino acid sequence set forth as residues 1-530 of the envelope glycoprotein of LAV.sub.MAL ; a purified or synthetic peptide having the amino acid sequence set forth as residues 34-530 of the envelope glycoprotein of LAV.sub.MAL and a purified or synthetic peptide having the amino acid sequence set forth as residues 531-877 of the envelope glycoprotein of LAV.sub.MAL, (b) reagents for the detection of the formation of antigen-antibody complex, and (c) a biological reference sample lacking antibodies recognized by said antigen, wherein the peptide, reagents,

and biological reference sample are present in an amount sufficient to perform the detection of antigen-antibody complex formed between said peptide and antibodies present in said biological reference sample.

L4 ANSWER 10 OF 13 USPATFULL
1998:75745 DNA fragments obtained from a novel human immunodeficiency virus designated LAV.sub.MAL.
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Sonigo, Pierre, Paris, France
Wain-Hobson, Simon, Montigny les Bretonneux, France
Montagnier, Luc, Le Plessis Robinson, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5773602 19980630
APPLICATION: US 1993-154397 19931118 (8)
PRIORITY: FR 1986-401380 19860623
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A novel human immunodeficiency virus type 1 (HIV-1) isolate, designated lymphadenopathy-associated virus strain MAL, or LAV.sub.MAL, was molecularly cloned and characterized. Nucleotide sequence analysis demonstrated that the viral genome of LAV.sub.MAL is 9229 nucleotides long. This retrovirus contains the canonical gag, pol, and env genes, as well as ancillary genes encoding Vif (or Q), Vpr (or R), Tat (or S), and Nef (or F). This virus differs significantly, at both the nucleotide and amino acid sequence levels, from prototypical HIV isolates (e.g., HTLV-III, LAV.sub.BRU, and ARV). DNA fragments corresponding to the various gene products and regulatory regions are disclosed. These fragments are useful, inter alia, as probes in diagnostic assays and for the generation of recombinant proteins.

CLM What is claimed is:
1. A DNA fragment having a nucleotide sequence selected from the group consisting of: a sequence having nucleotides 1 to 96, which is the long terminal repeat R region of LAV.sub.MAL ; a sequence having nucleotides 97 to 179, which is the 5' long terminal repeat U5 region of LAV.sub.MAL ; a sequence having nucleotides 8676 to 9133, which is the 3' long terminal repeat U3 region of LAV.sub.MAL ; a sequence having nucleotides 9134 to 9229, which is the 3' long terminal repeat U3 region of LAV.sub.MAL ; a sequence having nucleotides 5405 to 5620, which is the tat coding region of LAV.sub.MAL ; a sequence having nucleotides 5134 to 5421, which is the vpr coding region of LAV.sub.MAL ; a sequence having nucleotides 8380 to 9006, which is the nef coding region of LAV.sub.MAL ; a sequence having nucleotides 350 to 1864, which is the gag coding region of LAV.sub.MAL ; a sequence having nucleotides 1663 to 4668, which is the pol coding region of LAV.sub.MAL ; a sequence having nucleotides 5799 to 8375, which is the env coding region of LAV.sub.MAL ; a sequence having nucleotides 764 to 1501, which is the gag p25 coding region of LAV.sub.MAL ; a sequence having nucleotides 1502 to 1864, which is the gag p13 coding region of LAV.sub.MAL ; a sequence having nucleotides 5799 to 5885, which corresponds to amino acids 1-33 of the env coding region of LAV.sub.MAL ; a sequence having nucleotides 5886 to 7337, which corresponds to amino acids 34 to 530 of the gp110 env coding region of LAV.sub.MAL ; a sequence having nucleotides 5895 to 6176, which corresponds to amino acids 37 to 130 of the env coding region of LAV.sub.MAL ; a sequence having nucleotides 6399 to 6635, which corresponds to amino acids 211 to 289 of the env coding region of LAV.sub.MAL ; a sequence having nucleotides 7212 to 7337, which corresponds to amino acids 488 to 530 of the env coding region of LAV.sub.MAL ; a

sequence having nucleotides 7215 to 7604, which corresponds to amino acids 490 to 620 of the env coding region of LAV.sub.MAL ; and a sequence having nucleotides 7782 to 7844, which corresponds to amino acids 680 to 700 of the env coding region of LAV.sub.MAL.

2. The DNA fragment as claimed in claim 1, wherein said fragment is operatively linked to a promoter sequence.

3. A DNA fragment as claimed in claim 1, wherein said fragment has a nucleotide sequence having nucleotides 1 to 96, which is the long terminal repeat R region of LAV.sub.MAL.

4. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 97 to 179, which is the 5' long terminal repeat U5 region of LAV.sub.MAL.

5. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 8676 to 9133, which is the 3' long terminal repeat U3 region of LAV.sub.MAL.

6. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 9134 to 9229, which is the 3' long terminal repeat U3 region of LAV.sub.MAL.

7. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 5405 to 5620, which is the tat coding region of LAV.sub.MAL.

8. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 5134 to 5421, which is the vpr coding region of LAV.sub.MAL.

9. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 8380 to 9006, which is the nef coding region of LAV.sub.MAL.

10. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 350 to 1864, which is the gag coding region of LAV.sub.MAL.

11. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 1663 to 4668, which is the pol coding region of LAV.sub.MAL.

12. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 5799 to 8375, which is the env coding region of LAV.sub.MAL.

13. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 764 to 1501, which is the gag p25 coding region of LAV.sub.MAL.

14. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 1502 to 1864, which is the gag p13 coding region of LAV.sub.MAL.

15. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 5799 to 5885, which corresponds to amino acids 1-33 of the env coding region of LAV.sub.MAL.

16. A DNA fragment as claimed in claim 1, wherein said fragment has a

sequence having nucleotides 5886 to 7337, which corresponds to amino acids 34 to 530 of the gp110 env coding region of LAV.sub.MAL.

17. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 5895 to 6176, which corresponds to amino acids 37 to 130 of the env coding region of LAV.sub.MAL.

18. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 6399 to 6635, which corresponds to amino acids 211 to 289 of the env coding region of LAV.sub.MAL.

19. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 7212 to 7337, which corresponds to amino acids 488 to 530 of the env coding region of LAV.sub.MAL.

20. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 7215 to 7604, which corresponds to amino acids 490 to 620 of the env coding region of LAV.sub.MAL.

21. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 7782 to 7844, which corresponds to amino acids 680 to 700 of the env coding region of LAV.sub.MAL.

22. A recombinant vector comprising a DNA fragment of any one of claims 1-21.

23. A transformed host comprising the recombinant vector of claim 22.

L4 ANSWER 11 OF 13 USPATFULL
1998:48164 Diagnostic kits and methods for detecting antibodies to LAV viruses.
Alizon, Marc, Paris, France
Sonigo, Pierre, Paris, France
Wain-Hobson, Simon, Montigny les Bretonneux, France
Montagnier, Luc, Le Plessis Robinson, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5747242 19980505
APPLICATION: US 1995-466907 19950606 (8)
PRIORITY: EP 1986-401380 19860623
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A variant of a LAV virus, designated LAV.sub.ELI and cable of causing AIDS. The cDNA and antigens of the LAV.sub.ELI virus can be used for the diagnosis of AIDS an pre-AIDS.

CLM What is claimed is:
1. A method for the in vitro detection of an antibody directed against a lymphadenopathy associated virus in a human body fluid, comprising the steps of contacting said body fluid with an isolated or synthetic peptide, and then detecting the immunological reaction between said peptide and said antibody, wherein said isolated or synthetic peptide comprises an amino acid sequence that is a fragment of the following amino acid sequence: ##STR1## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises at least one amino acid sequence selected from the group consisting of amino-acyl residues 37-130, amino-acyl residues 211-289, amino-acyl

residues 488-530, amino-acyl residues 490-620, amino-acyl residues 680-700, amino-acyl residues 1-530, amino-acyl residues 34-530, and amino-acyl residues 531-877 of an envelope glycoprotein of LAV.sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with LAV.sub.BRU as set forth in FIG. 3.

2. The method of claim 1, wherein said amino acid sequence is selected from the group consisting of amino-acyl residues 37 to 130, 211 to 289, and 488 to 530.

3. The method of claim 1, wherein said amino acid sequence comprises amino-acyl residues 490 to 620 or 680 to 700.

4. The method of claim 1, wherein said amino acid sequence is selected from the group consisting of: amino-acyl residues 1 to 530; amino-acyl residues 34 to 530; and amino-acyl residues 531 to 877.

5. The method of claim 1, wherein said lymphadenopathy associated virus is LAV.sub.ELI.

6. The method of claim 1, wherein said contacting and detecting steps comprise: a) depositing a predetermined amount of said peptide into wells of a microplate; b) introducing increasing dilutions of said body fluid into said wells; c) incubating said microplate to allow the formation of antibody-peptide complexes; d) washing the microplate; e) adding to said wells a labeled antibody directed against immunoglobulins; and then f) determining whether an antigen-antibody complex has formed in said wells.

7. A method for the in vitro detection of an antibody directed against a lymphadenopathy associated virus in a human body fluid, comprising the steps of contacting said body fluid with an isolated or synthetic peptide, and then detecting the immunological reaction between said peptide and said antibody, wherein said isolated or synthetic peptide comprises an amino acid sequence that is a fragment of the following amino acid sequence: ##STR2## wherein, said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises a p25 peptide comprising amino-acyl residues 138-385 of gag protein of LAV.sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with LAV.sub.BRU as set forth in FIG. 3.

8. The method of claim 7, wherein said lymphadenopathy associated virus is LAV.sub.ELI.

9. The method of claim 7, wherein said contacting and detecting steps comprise: a) depositing a predetermined amount of said peptide into wells of a microplate; b) introducing increasing dilutions of said body fluid into said wells; c) incubating said microplate to allow the formation of antibody-peptide complexes; d) washing the microplate; e) adding to said wells a labeled antibody directed against immunoglobulins; and then f) determining whether an antigen-antibody complex has formed in said wells.

10. A method for the in vitro detection of an antibody directed against a lymphadenopathy associated virus in a human body fluid, comprising the steps of contacting said body fluid with an isolated or synthetic peptide, and then detecting the immunological reaction between said

peptide and said antibody, wherein said isolated or synthetic peptide comprises an amino acid sequence that is a fragment of the following amino acid sequence: ##STR3## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L, is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises a p13 peptide comprising amino-acyl residues 385-519 of gag protein of LAV.sub.ELL virus, and wherein the hyphens represent a gap introduced to align the sequence with LAV.sub.RM as set forth in FIG. 3.

11. The method of claim 10, wherein said lymphadenopathy associated virus is LAV.sub.ELI.

12. The method of claim 10, wherein said contacting and detecting steps comprise: a) depositing a predetermined amount of said peptide into wells of a microplate; b) introducing increasing dilutions of said body fluid into said wells; c) incubating said microplate to allow the formation of antibody-peptide complexes; d) washing the microplate; e) adding to said wells a labeled antibody directed against immunoglobulins; and then f) determining whether an antigen-antibody complex has formed in said wells.

13. A method for the in vitro detection of an antibody directed against a lymphadenopathy associated virus in a human body fluid, comprising the steps of contacting said body fluid with an isolated or synthetic peptide, and then detecting the immunological reaction between said peptide and said antibody, wherein said isolated or synthetic peptide comprises an amino acid sequence that is a fragment of the following amino acid sequence: ##STR4## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment is selected from the group consisting of amino-acyl residues 14-20, amino-acyl residues 50-59, amino-acyl residues 371-383, amino-acyl residues 410-430, and amino-acyl residues 536-557 of the pol protein of LAV.sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with LAV.sub.RM as set forth in FIG. 3.

14. The method of claim 13, wherein said lymphadenopathy associated virus is LAV.sub.ELI.

15. The method of claim 13, wherein said contacting and detecting steps comprise: a) depositing a predetermined amount of said peptide into wells of a microplate; b) introducing increasing dilutions of said body fluid into said wells; c) incubating said microplate to allow the formation of antibody-peptide complexes; d) washing the microplate; e) adding to said wells a labeled antibody directed against immunoglobulins; and then f) determining whether an antigen-antibody complex has formed in said wells.

16. A diagnostic kit for the in vitro detection of antibodies against a LAV virus, which kit comprises an antigen selected from the group consisting of the following: an isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR5## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, F is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is

lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises at least one amino acid sequence selected from the group consisting of amino-acyl residues 37-130, amino-acyl residues 211-289, amino-acyl residues 488-530, amino-acyl residues 490-620, amino-acyl residues 680-700, amino-acyl residues 1-530, amino-acyl residues 34-530, and amino-acyl residues 531-877 of an envelope glycoprotein of LAV.sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with LAV.sub.BRU as set forth in FIG. 3; an isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following, amino acid sequence: ##STR6## wherein, said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises a p25 peptide comprising amino-acyl residues 138-385 of gag protein of LAV.sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with LAV.sub.BRU as set forth in FIG. 3; an isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR7## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises a p13 peptide comprising amino-acyl residues 385-519 of gag protein of LAV.sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with LAV.sub.BRU as set forth in FIG. 3; and an isolated or synthetic peptide comprising an amino acid sequence having a fragment of the following amino acid sequence: ##STR8## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment is selected from the group consisting of amino-acyl residues 14-20, amino-acyl residues 50-59, amino-acyl residues 371-383, amino-acyl residues 410-430, and amino-acyl residues 536-557 of the pol protein of LAV.sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with LAV.sub.BRU as set forth in FIG. 3; a reagent or reagents for detecting a peptide-antibody complex; a biological reference material lacking antibodies that bind to said peptide or peptides; and a comparison sample comprising antibodies that bind to said peptide or peptides.

L4 ANSWER 12 OF 13 USPATFULL
91:59054 Variant of LAV viruses.
Alizon, Marc, Paris, France
Sonigo, Pierre, Paris, France
Wain-Hobson, Simon, Montigny les Bretonneux, France
Montagnier, Luc, Le Plessis Robinson, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5034511 19910723
APPLICATION: US 1987-38332 19870413 (7)
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A variant of a LAV virus, designated LAV.sub.ELI and capable of causing AIDS. The cDNA and antigens of the LAV.sub.ELI virus can be used for the diagnosis of AIDS and pre-AIDS.

CLM What is claimed is:

1. An isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR1## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises at least one amino acid sequence selected from the group consisting of amino-acyl residues 37-130, amino-acyl residues 211-289, amino-acyl residues 488-530, amino-acyl residues 490-620, amino-acyl residues 680-700, amino-acyl residues 1-530, amino-acyl residues 34-530, amino-acyl residues 531-877 of an envelope glycoprotein of LAV.sub.ELI virus.

2. An isolated or synthetic peptide as claimed in claim 1, wherein said amino acid sequence comprises a sequence selected from the group consisting of amino-acyl residues 37 to 130, 211 to 289, and 488 to 530.

3. An isolated or synthetic peptide as claimed in claim 1, wherein said amino acid sequence comprises amino-acyl residues 490 to 620 or 680 to 700.

4. An isolated or synthetic peptide as claimed in claim 1, wherein said amino acid sequence comprises a sequence selected from the group consisting of: amino-acyl residues 1 to 530; amino-acyl residues 34 to 530; and amino-acyl residues 531 to 877.

5. An immunogenic composition comprising an isolated or synthetic peptide as claimed in claim 1, and a physiologically acceptable carrier.

6. A diagnostic kit for the in vitro detection of antibodies against a lymphadenopathy associated virus comprising an isolated or synthetic peptide as claimed in claim 1, and a reagent for detecting the formation of peptide/antibody complex.

7. An isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR2## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p25 peptide comprising amino-acyl residues 138-385 of gag protein of LAV.sub.ELI virus.

8. An isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR3## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p13 peptide comprising amino-acyl residues 385-519 of gag protein of LAV.sub.ELI virus.

9. An isolated or synthetic peptide comprising an amino acid sequence: ##STR4## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine.

L4 ANSWER 13 OF 13 USPATFULL
91:54851 Variant of LAV viruses.
Alizon, Marc, Paris, France
Sonigo, Pierre, Paris, France
Wain-Hobson, Simon, Montigny Les Bretonneux, France
Montagnier, Luc, Le Plessis Robinson, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5030714 19910709
APPLICATION: US 1987-38330 19870413 (7)
PRIORITY: EP 1986-401380 19860623
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A variant of the LAV virus, designated LAV.sub.MAL and capable of causing AIDS. The cDNA and antigens of the LAV.sub.MAL virus can be used for the diagnosis of AIDS and pre-AIDS.

CLM What is claimed is:
1. An isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR1## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises at least one amino acid sequence selected from the group consisting of amino-acyl residue 37-130, amino-acyl residues 211-289, amino-acyl residues 488-530, amino-acyl residues 490-620, amino-acyl residues 680-700, amino-acyl residues 1-530, amino-acyl residues 34-530, amino-acyl residues 531-877 of an envelope glycoprotein of LAV.sub.MAL virus.

2. An immunogenic composition comprising an isolated or synthetic peptide as claimed in claim 1 and a physiologically acceptable carrier, wherein said immunogenic composition is capable of eliciting an immune response to said peptide in a host.

3. An immunogenic composition as claimed in claim 2, wherein said peptide is coupled to a physiologically acceptable and non-toxic carrier molecule that is capable of enhancing the immunogenicity of the peptide.

4. An immunogenic composition as claimed in claim 3, wherein said carrier molecule is a natural protein or a synthetic macromolecular carrier.

5. An immunogenic composition as claimed in claim 4, wherein said natural protein is selected from the group consisting of tetanus toxoid, ovalbumin, serum albumin, and hemocyanin.

6. An immunogenic composition as claimed in claim 4, wherein said synthetic macromolecular carrier is polylysine or poly(D-L

alanine)-poly(L-lysine).

7. The peptide of claim 1, wherein said peptide is a glycoprotein.

8. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 37-130 of the envelope glycoprotein of LAV.sub.MAL virus.

9. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 211-289 of the envelope glycoprotein of LAV.sub.MAL virus.

10. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 488-530 of the envelope glycoprotein of LAV.sub.MAL virus.

11. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 490-620 of the envelope glycoprotein of LAV.sub.MAL virus.

12. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 680-700 of the envelope glycoprotein of LAV.sub.MAL virus.

13. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 1-530 of the envelope glycoprotein of LAV.sub.MAL virus.

14. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 34-530 of the envelope glycoprotein of LAV.sub.MAL virus.

15. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 531-877 of the envelope glycoprotein of LAV.sub.MAL virus.

16. An isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR2## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p25 peptide comprising amino-acyl residues 138-385 of gag protein of LAV.sub.MAL virus.

17. An immunogenic composition comprising an isolated or synthetic peptide as claimed in claim 16 and a physiologically acceptable carrier, wherein immunogenic composition is capable of eliciting an immune response to said peptide in a host.

18. An isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR3## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p13 peptide comprising amino-acyl residues 385-519 of gag protein of LAV.sub.MAL

virus.

19. An immunogenic composition comprising an isolated or synthetic peptide as claimed in claim 18 and a physiologically acceptable carrier, wherein immunogenic composition is capable of eliciting an immune response to said peptide in a host.

20. An isolated or synthetic peptide comprising an amino acid sequence: ##STR4## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine.

L11 ANSWER 22 OF 36 USPATFULL
1998:98770 HIV-3 retrovirus antigen compositions.
De Leys, Robert, Grimbergen, Belgium
Vanderborght, Bart, Geel, Belgium
Saman, Eric, St. Niklaas, Belgium
Van Heuverswyn, Hugo, Laarne, Belgium
Innogenetics N.V., Ghent, Belgium (non-U.S. corporation)
US 5795743 19980818
APPLICATION: US 1995-486836 19950607 (8)
PRIORITY: EP 1988-109200 19880609
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Described is a new variety of retrovirus designated HIV-3 samples of which are deposited in the European Collection of Animal Cell Cultures (ECACC) under V88060301. Further described are antigens obtained from the virus, particularly proteins p12, p16, p25 and glycoproteins gp41 and gp120 to be used in the diagnosis of ARC or AIDS caused by HIV-3. Immunogenic compositions to be used as vaccines contain an envelope glycoprotein of HIV-3 such as gp41 or gp120.

CLM What is claimed is:
1. A composition comprising at least one protein or glycoprotein of HIV-3 retrovirus, said retrovirus (also known as HIV-1 subtype O virus) having the morphological and immunological characteristics of any of the retroviruses deposited in the European Collection of Animal Cell Cultures under V88060301.

2. The composition of claim 1 wherein the composition comprises a total extract or lysate of HIV-3 retrovirus.

3. The composition of claim 1 wherein the composition comprises at least one of the internal core proteins of HIV-3 retrovirus selected from the group consisting of p12, p16 and p25.

4. The composition of claim 1 wherein the composition comprises at least one of the envelope glycoproteinsof HIV-3 retrovirus selected from the group consisting of gp41 and gp120.

5. A purified antigen of HIV-3 retrovirus (also known as HIV-1 subtype O virus) providing a single band in polyacrylamide gel electrophoresis, and containing an epitope that is immunoreactive with patient sera containing anti-HIV-3 antibodies.

6. A purified antigen selected from the group consisting of p12, p16,

p25, gp41 and gp120, wherein the antigen is isolated from HIV-3 retrovirus (also known as HIV-1 subtype O virus).

7. The antigen of claim 6 wherein the antigen is the p12 protein of HIV-3, obtained by subjecting an extract or lysate of HIV-3 to gel electrophoresis and isolating the p12 protein from the gel.

8. The antigen of claim 6 wherein the antigen is the p16 protein of HIV-3, obtained by subjecting an extract or lysate of HIV-3 to gel electrophoresis and isolating the p16 protein from the gel.

9. The antigen of claim 6 wherein the antigen is the p25 protein of HIV-3, obtained by subjecting an extract or lysate of HIV-3 to gel electrophoresis and isolating the p25 protein from the gel.

10. The antigen of claim 6 wherein the antigen is the gp41 protein of HIV-3, obtained by subjecting an extract or lysate of HIV-3 to gel electrophoresis and isolating the gp41 protein from the gel.

11. The antigen of claim 6 wherein the antigen is the gp120 protein of HIV-3, obtained by subjecting an extract or lysate of HIV-3 to gel electrophoresis and isolating the gp120 protein from the gel.

12. A method for the production of antigens of HIV-3 retrovirus (also known as HIV-1 subtype O virus) comprising the steps of lysing the retrovirus and recovering the lysate containing HIV-3 antigens.

L11 ANSWER 25 OF 36 USPATFULL
1998:88668 Nucleotide sequences derived from the genome or retroviruses of the HIV-1, HIV-2, and SIV type, and their uses in particular for the amplification of the genomes of these retroviruses and for the in vitro diagnosis of the diseases due to these viruses.
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Montagnier, Luc, Le Plessis-Robinson, France
Institut Pasteur, Paris, France (non-U.S. corporation) Institut National de la Sante et de la Recherche Medicale, Paris, France (non-U.S. corporation)
US 5786177 19980728
APPLICATION: US 1997-895231 19970716 (8)
PRIORITY: FR 1989-7954 19890602
FR 1989-12371 19890920
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to nucleotidic sequences derived from genomes of the HIV-1 type virus, or from genomes of the HIV-2 type virus, or of the SIV type virus, and their applications, especially as oligonucleotidic initiators of implementation of an (in vitro) method for the diagnosis of the infection of an individual by a virus of the HIV-1 and/or HIV-2 type.

CLM What is claimed is:
1. A method for the preparation of a polypeptide encoded by a region of the HIV or SIV genome, said method comprising: a) amplifying the nucleic acid encoding said polypeptide with at least two primers, wherein said first primer is complementary to a region of nucleotides of the nucleic

acid of said genome, said second primer is complementary to a region of nucleotides of the strand of DNA complementary to said nucleic acid of said genome, wherein said regions of nucleotides are separated by about 100 to about 1100 base pairs when said complementary strands are hybridized to form one double-stranded nucleic acid, and said primer is selected from the group consisting of: nucleotides 900-881, 1385-1369, 1388-1369, and 2039-2021 of a nucleic acid sequence complementary to the gag gene of HIV-1 Bru; nucleotides 916-897, 1419-1403, 1421-1403, and 2073-2055 of a nucleic acid sequence complementary to the gag gene of HIV-1 Mal; nucleotides 900-881, 1385-1369, 1388-1369, and 2042-2024 of a nucleic acid sequence complementary the gag gene of HIV-1 Eli; nucleotides 1212-1193, 1703-1687, 1706-1687, and 2349-2329 of a nucleic acid sequence complementary to the gag gene of HIV-2 ROD; nucleotides 1176-1157, 1667-1651, 1670-1651, and 2381-2299 of a nucleic acid sequence complementary to the gag gene of SIV-MAC; nucleotides 5870-5849 of a nucleic acid sequence complementary to the vpr gene of HIV-1 Bru; nucleotides 5865-5844 of a nucleic acid sequence complementary to the vpr gene of HIV-1 Mal; nucleotides 5834-5813 of a nucleic acid sequence complementary to the vpr gene of HIV-1 Eli; nucleotides 6551-6531 of a nucleic acid sequence complementary to the vpr gene of HIV-2 ROD; nucleotides 6454-6431 of a nucleic acid sequence complementary to the vpr gene of SIV-MAC; nucleotides 2643-2620, 3361-3339, 4207-4186, and 5011-4992 of a nucleic acid sequence complementary to the pol gene of HIV-1 Bru; nucleotides 2638-2615, 3356-3334, 4202-4181, and 5006-4987 of a nucleic acid sequence complementary to the pol gene of HIV-1 Mal; nucleotides 2607-2584, 3325-3303, 4171-4150, and 4975-4956 of a nucleic acid sequence complementary to the pol gene of HIV-1 Eli; nucleotides 2994-2971, 3712-3690, 4555-4534, and 5359-5340 of a nucleic acid sequence complementary to the pol gene of HIV-2 ROD; nucleotides 3010-2887, 3628-3606, 4471-4450, and 5275-5256 of a nucleic acid sequence complementary to the pol gene of SIV-MAC; nucleotides 9564-9542 and 9956-9933 of a nucleic acid sequence complementary to the nef2 gene of HIV-2 ROD; nucleotides 9538-9516 and 9839-9870 of a nucleic acid sequence complementary to the nef2 gene of SIV-MAC; nucleotides 5775-5754 and 6082-6061 of a nucleic acid sequence complementary to the vif2 gene of HIV-2 ROD; nucleotides 5691-5670 and 5995-5974 of a nucleic acid sequence complementary to the vif2 gene of SIV-MAC nucleotides 6228-6208 of a nucleic acid sequence complementary to the vpx gene of HIV-2 ROD; nucleotides 6141-6121 of a nucleic acid sequence complementary to the vpx gene of SIV-MAC; nucleotides 6930-6905, 7384-7360, 7857-7832, 8869-8844, and nucleotides 8242-8224 of a nucleic acid sequence complementary to the env gene of HIV-1 Bru; nucleotides 6928-6903, 7373-7349, 7846-7821, 8861-8836, and 8231-8213 of a nucleic acid sequence complementary to the env gene of HIV-1 Mal; nucleotides 6885-6860, 7330-7306, 7800-7775, 8812-8787, and 8185-8167 of a nucleic acid sequence complementary to the env gene of HIV-1 Eli; nucleotides 9136-9116 and 9503-9483 of a nucleic acid sequence complementary to the nef1 gene of HIV-1 Bru; nucleotides 9137-9117 and 9505-9484 of a nucleic acid sequence complementary to the nef1 gene of HIV-1 Mal; nucleotides 9082-9062 and 9449-9428 of a nucleic acid sequence complementary to the nef1 gene of HIV-1 Eli; nucleotides 5405-5383 and 5675-5653 of a nucleic acid sequence complementary to the vif1 gene of HIV-1 Bru; nucleotides 5400-5378 and 5670-5648 of a nucleic acid sequence complementary to the vif1 gene of HIV-1 Mal and nucleotides 5369-5347 and 5639-5617 of a nucleic acid sequence

complementary to the vif1 gene of HIV-1 Eli; nucleotides 6343-6321 of a nucleic acid sequence complementary to the vpu gene of HIV-1 Bru; nucleotides 6338-6316 of a nucleic acid sequence complementary to the vpu gene of HIV-1 Mal; and nucleotides 6307-6285 of a nucleic acid sequence complementary to the vpu gene of SIV-MAC; b) introducing said amplified nucleotide sequence into a vector; c) transforming a host cell with said vector; and d) placing said transformed host cell in culture and recovering said polypeptide from said culture.

2. A method for the preparation of a polypeptide encoded by a region of the HIV or SIV genome, said method comprising: a) amplifying the nucleic acid encoding said polypeptide with at least two primers, wherein said first primer is complementary to a region of nucleotides of the nucleic acid of said genome, said second primer is complementary to a region of nucleotides of the strand of DNA complementary to said nucleic acid of said genome, wherein said regions of nucleotides are separated by about 100 to about 1100 base pairs when said complementary strands are hybridized to form one double-stranded nucleic acid, and said primer is selected from the group consisting of:

MMyl: TGG .....
AA

b) introducing said amplified nucleotide sequence into a vector; c) transforming a host cell with said vector; and d) placing said transformed host cell in culture and recovering said polypeptide from said culture.

L18 ANSWER 3 OF 57 MEDLINE
1999089502 Document Number: 99089502. PubMed ID: 9874106. Molecular variants of HIV-1 and their impact on vaccine development. Quinn T C. (Laboratory of Immunoregulation, National Institute of Allergy and Infectious Diseases, Bethesda, Maryland, USA.) INTERNATIONAL JOURNAL OF STD AND AIDS, (1998) 9 Suppl 1 2.
Journal code: 9007917. ISSN: 0956-4624.
Report No.: PIP-139272; POP-00284471. Pub. country: ENGLAND: United Kingdom. Language: English.

AB The global HIV pandemic is heterogenous and dynamic, and comprised of many subepidemics in different geographic locations and populations, each with distinctive features such as risk factors for transmission, clinical presentation of disease, and viral subtypes in circulation. The genetic sequencing of HIV isolates has identified 2 major groups of HIV-1 designated group M (main) and group O (outlier). 10 different subtypes have been documented within the M group, subtypes A through J, comprising more than 95% of all HIV infections worldwide. Group O viruses have not been subtyped and are of limited distribution, found mainly in west Africa and with sporadic reports in Europe and the US. HIV-1 group M viruses have been the most intensely studied due to their global prevalence, with the best characterized subtype being subtype B, the predominant subtype in Europe and North America. The capacity of HIV subtypes to recombine allows rapid and marked genetic change. The greatest genetic variation in HIV-1 has been detected in central Africa, the area with the greatest density and duration of infection. Subtype C has the greatest frequency of any subtype globally, with epidemics in South Africa, East Africa, and India. The diverse molecular variation in the HIV genome among viral subtypes presents an obstacle to the development of an effective vaccine. The need to explore the development of both envelope -based and multi-gene-based vaccines is noted.

L20 ANSWER 12 OF 12 MEDLINE
95074874 Document Number: 95074874. PubMed ID: 7983718. Genetic diversity of the envelope glycoprotein from human immunodeficiency virus type 1 isolates of African origin. Louwagie J; Janssens W; Mascola J; Heyndrickx L; Hegerich P; van der Groen G; McCutchan F E; Burke D S. (Henry M. Jackson Foundation Research Laboratory, Rockville, Maryland.) JOURNAL OF VIROLOGY, (1995 Jan) 69 (1) 263-71.
Journal code: 0113724. ISSN: 0022-538X. Pub. country: United States.
Language: English.

AB The genetic diversity of the envelope glycoprotein of human immunodeficiency virus type 1 (HIV-1) isolates was studied. HIV-1 isolates were obtained from eight countries in Africa: Djibouti, Gabon, Kenya, Senegal, Somalia, Uganda, Zaire, and Zambia. The DNA sequences encoding the complete HIV-1 envelope protein were PCR amplified and sequenced. Phylogenetic relationships among the 21 sequences from this study and the 32 previously published full-length env HIV-1 sequences were determined. Twenty of the newly sequenced African isolates could be assigned to envelope subtypes A, C, D, and G. One isolate, collected in Zambia, did not belong to any of the eight previously described subtypes and may represent a prototype sequence of its envelope subtype. The phylogenetic classification of these isolates was strongly supported by bootstrapping and the congruence of trees generated by either

distance methods or maximum parsimony analysis. The data presented in this study confirm the existence of several genetic subtypes within the global HIV epidemic and broaden the genetic variability previously observed for envelope subtypes. The geographic spread of different subtypes was shown to be substantial, and the notion of cocirculation of subtypes was reinforced.

L20 ANSWER 7 OF 12 MEDLINE
96014957 Document Number: 96014957. PubMed ID: 7576318. The evolving molecular epidemiology of HIV-1 envelope subtypes in injecting drug users in Bangkok, Thailand: implications for HIV vaccine trials. Kalish M L; Baldwin A; Raktham S; Wasi C; Luo C C; Schochetman G; Mastro T D; Young N; Vanichseni S; Rubsamen-Waigmann H; +. (Division of HIV/AIDS, Centers for Disease Control and Prevention, Atlanta, Georgia 30333, USA.) AIDS, (1995 Aug) 9 (8) 851-7.
Journal code: 8710219. ISSN: 0269-9370.
Report No.: PIP-107478; POP-00244693. Pub. country: United States.
Language: English.

AB OBJECTIVE: To genetically characterize HIV-1 strains in injecting drug users (IDU) in Bangkok, Thailand in 1994, and compare these with strains found earlier in Thai IDU; such information is essential for HIV-1 vaccine development and evaluation. METHODS: Peripheral blood mononuclear cells were collected from 84 IDU attending 14 drug treatment clinics in Bangkok in 1994. DNA was amplified using a nested polymerase chain reaction (PCR) procedure and sequenced directly (without cloning) from the PCR products. The V3 and flanking regions (345 nucleotides) of the env gene were analyzed using a neighbor-joining tree. RESULTS: Only one (1%) strain was a typical subtype B virus, 69 (82%) were genetically distinct subtype B' viruses (Thai B), and 14 (17%) were subtype E strains (Thai A). Persons with recently acquired infection were more likely to have subtype E viruses ($P < 0.001$) than those in our 1991 survey, who were more likely to have subtype B' viruses. Pairwise intra-subtype differences within subtypes E and B' were 5.3 and 4.3%, respectively, compared with 3.4 and 3.5% among strains collected in 1991 in Thailand. CONCLUSION: The genetic diversity within subtypes B' and E in Thailand and the proportion of new infections due to subtype E viruses among Bangkok IDU are increasing significantly. These data highlight the importance of monitoring the molecular epidemiology of HIV-1 in populations being considered for HIV-1 vaccine trials.

L20 ANSWER 1 OF 12 MEDLINE
96353297 Document Number: 96353297. PubMed ID: 8748017. Revealing the history of infectious disease epidemics through phylogenetic trees. Holmes E C; Nee S; Rambaut A; Garnett G P; Harvey P H. (Wellcome Centre for the Epidemiology of Infectious Disease, Department of Zoology, University of Oxford, U.K.) PHILOSOPHICAL TRANSACTIONS OF THE ROYAL SOCIETY OF LONDON. SERIES B: BIOLOGICAL SCIENCES, (1995 Jul 29) 349 (1327) 33-40.
Journal code: 7503623. ISSN: 0962-8436. Pub. country: ENGLAND: United Kingdom. Language: English.

AB Phylogenetic trees play an increasing role in molecular epidemiology, where they have been used to understand the forces that shape patterns of viral sequence diversity. Phylogenetic trees can also be used to trace the dynamics of viral transmission within populations. Case studies document the worldwide spread of Human Immunodeficiency Virus type 1 (HIV-1) and hepatitis C virus (HCV). Despite similarities between these viruses, especially in their transmission routes, they are shown to have very different epidemiological histories. A possible reason

for the difference is that HCV has coexisted longer with human populations.

L21 ANSWER 11 OF 15 MEDLINE
93290931 Document Number: 93290931. PubMed ID: 8512752. Sequence analysis of the gp120 region of the env gene of Ugandan human immunodeficiency proviruses from a single individual. Bruce C; Clegg C; Featherstone A; Smith J; Oram J. (Centre for Applied Microbiology and Research, Public Health Laboratory Service, Porton Down, Salisbury, England.) AIDS RESEARCH AND HUMAN RETROVIRUSES, (1993 Apr) 9 (4) 357-63. Journal code: 8709376. ISSN: 0889-2229. Report No.: PIP-092409; POP-00229530. Pub. country: United States. Language: English.

AB DNA sequences encoding the surface glycoprotein gp120 of the human immunodeficiency virus type 1 (HIV-1) were amplified by the polymerase chain reaction (PCR) from peripheral blood mononuclear cells obtained from a Ugandan AIDS patient. The PCR-amplified DNA was cloned into a phagemid vector and nine clones sequenced. The gp120 sequences of the proviruses were similar to that of the Zairian isolate HIV-JY1 and unlike that of another Ugandan provirus, U455. Six of the clones were closely related to each other (maximum nucleotide sequence divergence 1.9%), and had a V3 amino acid sequence similar to that frequently seen in recent isolates from Uganda. Two others formed a second group that diverged from the first by an average of 6.0% at the nucleotide level, resulting in a 12.5% divergence of amino acid sequence. These divergent clones had extensive amino acid sequence changes not only in the V3 region, which was highly atypical, but also in V1 and V4, and to a lesser extent in V2 and V5. A further proviral clone had a sequence intermediate between those of the other two groups of clones.

L21 ANSWER 3 OF 15 MEDLINE
94107601 Document Number: 94107601. PubMed ID: 8280481. Diversity of V3 region sequences of human immunodeficiency viruses type 1 from the central African Republic. Murphy E; Korber B; Georges-Courbot M C; You B; Pinter A; Cook D; Kieny M P; Georges A; Mathiot C; Barre-Sinoussi F; +. (Public Health Research Institute, New York, New York 10016.) AIDS RESEARCH AND HUMAN RETROVIRUSES, (1993 Oct) 9 (10) 997-1006. Journal code: 8709376. ISSN: 0889-2229. Report No.: PIP-094750; POP-00230645. Pub. country: United States. Language: English.

AB Nucleotide sequences of the central portion of gp120, including the third hypervariable (V3) loop, were obtained from lymphocytes cocultivated with SupT1 cells from 29 AIDS patients in Bangui, Central African Republic. These sequences displayed significantly greater diversity (average distance, 23%) than has been previously observed in isolates from comparably restricted geographical areas. Isolates belonging to four major subtypes of HIV-1 were found; the only subtype not represented was the North American/European subtype B. Unlike the situation in Zaire and Uganda, where subtypes A and D account equally for virtually all isolates of HIV-1, the predominant subtypes in the Central African Republic, accounting for two-thirds of the isolates, were subtypes A (10 isolates) and E (9 isolates). Subtype E represents a group of variants that have previously been found only in Thailand. Only one isolate belonging to subtype D was found. Also recovered were two isolates of subtype C, a subtype associated with southern African and Indian isolates

but not previously detected in central Africa. These isolates, although clearly clustering with subtype C, formed a distinct subset, differing from one another by 8.8% and from the Indian and South African subtype C isolates by an average of 22.5%. High interpatient, intrasubtype variation was also seen among the CAR subtype A (average pairwise difference, 19.3%) and subtype E (10.9%) isolates. The diversity of V3 sequences in this set has implications for immunization protocols that rely on the recognition of V3. This study underscores the necessity of basing intervention strategies on knowledge of the particular sequences present in the target population or geographical area.

L22 ANSWER 9 OF 9 MEDLINE
96093894 Document Number: 96093894. PubMed ID: 7576915. Seroreactivity of analogous antigenic epitopes in glycoprotein 120 expressed in HIV -1 subtypes A, B, C, and D. Pestano G A; Hosford K S; Spira A I; Riley J; Xie J M; Sewankambo N; Brown L; Ho D D; Boto W M. (Department of Biology, City College of the City University of New York, New York 10031, USA.) AIDS RESEARCH AND HUMAN RETROVIRUSES, (1995 May) 11 (5) 589-96. Journal code: 8709376. ISSN: 0889-2229.
Report No.: PIP-112176; POP-00251446. Pub. country: United States.
Language: English.

AB This article describes the impact of sequence variation on the distribution and seroreactivity of linear antigenic epitopes in gp120 encoded in new Ugandan HIV-1 clones from subtypes A, C, and D, and in North American clones from the B subtype. A region of the env gene encoding the C2 to V5 domains was PCR amplified from the lysates of peripheral blood leukocytes or from short-term cultured isolates. Computer-assisted analyses were conducted on the amino acid sequences to determine the distribution of surface structures in gp120. Despite marked sequence diversity, eight analogous epitopes were predicted for all clades of the virus analyzed. Synthetic peptides comprising the putative principal neutralizing determinant E2[V3], and other B cell epitopes E3[V3-V4], E4[V3-V4], E7[C3], and E8[V5], from a seroprevalent Ugandan isolate, AUG06c, were tested in ELISA for antigenicity with sera from Uganda, New York, and Thailand. Variable magnitudes of seroreactivity were observed for all of the peptides tested. However, a significantly higher degree of serum cross-reactivity was detected with the V3 loop peptide. ELISA reactivities of the same serum panel indicated that V3 loop peptides containing the apical residues GPGR (clones AUG06c and BRT3) or GPGQ (CUG045 and DUG044) were more antigenic and display extensive cross-reactivity as compared to analogous peptides comprising GLGQ (DUG23c), GQGQ (DUG042), or GPWG (BRT1). BETATURN analysis of the divergent V3 loop apical residues showed a good correlation of probable beta-turn occurrence with strong seroreactivity. These findings suggest that the major antigenic specificities in the divergent clades of HIV-1 are well conserved.(ABSTRACT TRUNCATED AT 250 WORDS)

L23 ANSWER 1 OF 1 MEDLINE
95127298 Document Number: 95127298. PubMed ID: 7545972. Genetic and antigenic variability of HIV type 1 in Brazil. Couto-Fernandez J C; Janssens W; Heyndrickx L; Motte J; Fransen K; Peeters M; Delaporte E; Galvao-Castro B; Piot P; van der Groen G. (Advanced Public Health Laboratory, Centro de Pesquisas Goncalo, Fundacao Oswaldo Cruz, Bahia CEP, Brazil.) AIDS RESEARCH AND HUMAN RETROVIRUSES, (1994 Sep) 10 (9) 1157-63. Journal code: 8709376. ISSN: 0889-2229.
Report No.: PIP-103595; POP-00240117. Pub. country: United States.
Language: English.

AB Six Brazilian strains of human immunodeficiency virus type 1 (HIV-1) were isolated from infected individuals residing in different regions of Brazil between 1987 and 1989. Phylogenetic analysis based on an 860-base pair env fragment, including V3, V4, V5, and the beginning of gp41, classified the Brazilian strains significantly in genotype B, with interhost distances between 5.9 and 13.1% (mean value, 10%). Amino acid sequence analysis of the V3 loop revealed that three strains contained the North American/European GPGR motif as the tip of the loop whereas in the other three strains proline (P) was substituted by tryptophan (W), methionine (M), or phenylalanine (F). A consensus peptide, Bra-cons, was designed containing GWGR as the tip of the loop. Serological reactivity to the Bra-cons peptide and other V3 peptides (MN, SF2, HBX2, RF, MAL, ELI, Z6, and a Cote d'Ivoire peptide, CI-cons) was compared for 114 HIV-1-positive sera from Rio de Janeiro. Sixty-nine sera (60.5%) reacted with peptides belonging to genotype B, of which 10 sera also reacted with peptides belonging to genotype A (n = 7) and D (n = 3). Eighteen sera (15.8%) had binding antibodies to the Bra-cons peptide. A high number of sera (n = 43; 37.7%) had no antibodies to any of the V3 peptides tested. This result suggests that HIV-1 variants with aberrant V3 loops may circulate in Rio de Janeiro.